

Eugene Shakhnovich

List of Publications by Year in descending order

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35
papers

3,443
citations

471509

17
h-index

434195

31
g-index

40
all docs

40
docs citations

40
times ranked

2517
citing authors

#	ARTICLE	IF	CITATIONS
1	Development of antibacterial compounds that constrain evolutionary pathways to resistance. ELife, 2021, 10, .	6.0	12
2	Cotranslational folding allows misfolding-prone proteins to circumvent deep kinetic traps. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 1485-1495.	7.1	44
3	Validation of DBFOLD: An efficient algorithm for computing folding pathways of complex proteins. PLoS Computational Biology, 2020, 16, e1008323.	3.2	11
4	Stability of the Influenza Virus Hemagglutinin Protein Correlates with Evolutionary Dynamics. MSphere, 2018, 3, .	2.9	31
5	Exploring the Mutational Robustness of Nucleic Acids by Searching Genotype Neighborhoods in Sequence Space. Journal of Physical Chemistry Letters, 2017, 8, 407-414.	4.6	11
6	Rational Design of Novel Allosteric Dihydrofolate Reductase Inhibitors Showing Antibacterial Effects on Drug-Resistant <i>Escherichia coli</i> Escape Variants. ACS Chemical Biology, 2017, 12, 1848-1857.	3.4	22
7	Benchmarking Inverse Statistical Approaches for Protein Structure and Design with Exactly Solvable Models. PLoS Computational Biology, 2016, 12, e1004889.	3.2	43
8	Searching the Sequence Space for Potent Aptamers Using SELEX in Silico. Journal of Chemical Theory and Computation, 2015, 11, 5939-5946.	5.3	27
9	The interface of protein structure, protein biophysics, and molecular evolution. Protein Science, 2012, 21, 769-785.	7.6	188
10	Soluble oligomerization provides a beneficial fitness effect on destabilizing mutations.. Nature Precedings, 2011, , .	0.1	0
11	Topology of protein interaction network shapes protein abundances and strengths of their functional and nonspecific interactions. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4258-4263.	7.1	94
12	Protein folding roller coaster, one molecule at a time. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 11823-11824.	7.1	4
13	Protein Folding Thermodynamics and Dynamics:Â Where Physics, Chemistry, and Biology Meet. Chemical Reviews, 2006, 106, 1559-1588.	47.7	332
14	On the origin and highly likely completeness of single-domain protein structures. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 2605-2610.	7.1	182
15	Protein structure and evolutionary history determine sequence space topology. Genome Research, 2005, 15, 385-392.	5.5	82
16	Phase Transformations and Orientational Ordering in Chemically Disordered Polymers â€” a Modern Primer. , 2004, , 455-484.		0
17	Field theory and segmental alignment analysis for a solution of sequence disordered liquid crystalline polymers. Journal of Chemical Physics, 2002, 116, 3134-3140.	3.0	1
18	Exotic phase transitions in disordered globular networks. Journal of Chemical Physics, 2001, 114, 10968-10976.	3.0	2

#	ARTICLE	IF	CITATIONS
19	Protein Folding Theory: From Lattice to All-Atom Models. Annual Review of Biophysics and Biomolecular Structure, 2001, 30, 361-396.	18.3	326
20	Evolutionary conservation of the folding nucleus ¹ Edited by A. R. Fersht. Journal of Molecular Biology, 2001, 308, 123-129.	4.2	116
21	Orientational ordering in sequence-disordered liquid crystalline polymers. Chemical Physics Letters, 2000, 325, 323-329.	2.6	4
22	Freezing in polyampholytes globules: Influence of the long-range nature of the interaction. Journal of Chemical Physics, 1999, 111, 772-785.	3.0	8
23	On the role of conformational geometry in protein folding. Journal of Chemical Physics, 1999, 111, 10375-10380.	3.0	28
24	Disordered heteropolymers with cross-links " phase diagram and conformational transitions. Chemical Physics Letters, 1999, 303, 355-362.	2.6	4
25	Factors that affect the folding ability of proteins. , 1999, 35, 34-40.		45
26	A strategy for detecting the conservation of folding-nucleus residues in protein superfamilies. Folding & Design, 1998, 3, 239-251.	4.5	49
27	Phase diagram analysis of random heteropolymers with composition specific and quenched cross-links. Journal of Chemical Physics, 1998, 109, 2947-2958.	3.0	7
28	Frozen phases with re-entrant transition for random heteropolymers with composition specific and annealed cross-links. Journal of Chemical Physics, 1997, 107, 1247-1258.	3.0	7
29	Protein Dynamics. , 1996, , 113-126.		0
30	Protein dynamics: From the native to the unfolded state and back again. Molecular Engineering, 1995, 5, 55-70.	0.2	1
31	Protein Dynamics: From the Native to the Unfolded State and Back Again. Jerusalem Symposia on Quantum Chemistry and Biochemistry, 1995, , 69-84.	0.2	5
32	How does a protein fold?. Nature, 1994, 369, 248-251.	27.8	934
33	Statistical mechanics of proteins with "evolutionary selected"™ sequences. Physical Review E, 1994, 50, 1303-1312.	2.1	69
34	Kinetics of Protein Folding. Journal of Molecular Biology, 1994, 235, 1614-1636.	4.2	513
35	Enumeration of all compact conformations of copolymers with random sequence of links. Journal of Chemical Physics, 1990, 93, 5967-5971.	3.0	240